UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/997,610	11/29/2001	Brian A. Fox	00-96	7389

7590 07/17/2002

Jennifer K. Johnson, J.D.
ZymoGenetics, Inc.
1201 Eastlake Avenue East
Seattle, WA 98102

EXAMINER
SNEDDEN, SHERIDAN

ART UNIT	PAPER NUMBER
1653	

DATE MAILED: 07/17/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/997,610	FOX ET AL.	
	Examiner	Art Unit	
	Sheridan K Snedden	1653	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____ .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) 1-21 is/are pending in the application.

4a) Of the above claim(s) 1-5 and 16-21 is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) 6-15 is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____ .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

Applicant's election of Invention II, Claims 6-15 is acknowledged. Election was made **without** traverse in Paper No. 6.

Priority

Applicant's claim for domestic priority under 35 U.S.C. 119(e) is acknowledged. However, the provisional application upon which priority is claimed fails to provide adequate support under 35 U.S.C. 112 for claim 11 of this application. The claim recites "SEQ ID NO: 7," which is not disclosed in the provisional application upon which priority is claimed.

Information Disclosure Statement

The listing of references in the specification is not a proper information disclosure statement. 37 CFR 1.98(b) requires a list of all patents, publications, or other information submitted for consideration by the Office, and MPEP § 609 A(1) states, "the list may not be incorporated into the specification but must be submitted in a separate paper." Therefore, unless the references have been cited by the examiner on form PTO-892, they have not been considered.

Specification

The disclosure is objected to because of the following informalities:

1. The reference cited on page 1, line 36 is incomplete. See also page 21, line 3.
2. The sequence disclosed on page 18 line 34 is not in compliance with 37 CFR 1.822 (d) which clearly states that any amino acid sequence shall be listed using the three-letter abbreviation with the first letter as an upper case character

Appropriate correction is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 6, 8, 11, 12 and dependent claims thereto are rejected under 35 U.S.C. 101 because the claimed invention lacks patentable utility. The above claims are directed to an isolated nucleic acid encoding a polypeptide of SEQ ID NO: 2, host cells, expression vectors and a method for producing the polypeptide of SEQ ID NO: 2, identified in the specification as Zarcp13. The nucleic acid above is disclosed as have utility in the detection of Zarcp13 gene expression (page 62, line 20), in the production of Zarcp13 polypeptide and as having therapeutic use (page 85, line 21). Of the above uses, none provide a specific or substantial asserted utility or a well established utility. Basic research, such as studying the properties of the claimed product itself or the mechanisms in which the material is involved, such as gene expression, do not constitute specific or substantial utilities. The therapeutic methods disclosed in the specification teach the treatment of unspecified disease or condition. Specifically, the specification merely states that the Zarcp13 nucleic acids may be provided to subjects in need of Zarcp13 treatment. Neither the specification nor the art of record disclose any diseases or conditions caused or exacerbated by Zarcp13. The asserted utility in this case essentially is a method of treating an unspecified, undisclosed disease or condition, which does not define a "real world" context of use. Treating an unspecified, undisclosed disease or condition would require or constitute carrying out further research to identify or reasonably confirm a "real world" context of use.

Additionally, the use of the nucleic acid in the method of making a polypeptide that itself has no specific and substantial asserted or well established utility is itself not specific and

substantial or well establish. The specification as filed does not disclose or provide any evidence that points to an activity for the protein and furthermore there is no art of record that discloses or suggests any activity for the claimed protein. The specification discloses the Zarcp13 polypeptide as having potential use, or that may be evaluated for such potential use, as a modulator of energy balance and cellular metabolic reactions (page 74, line 15); as a antimicrobial (page 77, line 21); as a modulator of calcium ion concentration, muscle contraction, hormone secretion DNA synthesis or cell growth, etc (page77, line 35); as an inducer of platelet aggregation (page 76, line 21); as having therapeutic use thereof (page 83, line 3); and as having an educational use (page 84, line 20). Further experimentation is required to identify a specific and substantial use for the polypeptide as only prophetic uses not yet evaluated are disclosed in the specification. Furthermore, the non-prophetic uses disclosed for the polypeptide, *e.g.* educational purposes, do not show specific utility as it states a general use of all polypeptides.

Thus, the claimed polynucleotide encoding protein is not supported by either a specific and substantial asserted utility or a well established utility as to the above because the specification fails to assert any well established utility for the protein and neither the specification as filed nor any art of record disclose or suggest any activity for the protein such that any utility would be well established for the protein.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 6, 8, 11, 12 and dependent claims thereto are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific or substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 6-15 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 6 is indefinite because each number of the Markush group recites "comprising." In item (a) the polypeptide "comprises" residues "19-45 of SEQ ID NO: 2," but comprises is open ended and can include residues 1-459 of SEQ ID NO: 2. Similarly, each recited member of (b) through (h) are similarly indefinite because it is not apparent how each member of the Markush group is mutually exclusive one from the other and because each item (a) through (h) overlap each other.

Claim 7 is indefinite as to "moiety" (singular) and the members recited in the Markush group (all plural). In addition, it is unclear in the claim what the common feature of each moiety is or is not supposed to be or have been.

Claim 8 is indefinite as to "portion" as to what is or is not the "a first portion" and the "a second portion." Is "portion " all or only part of items (a) through (g)? In addition, as to the "a second portion," does or does it not include a second or third of "a first portion" as "the second

portion comprising another polypeptide" does not preclude same when "another" is interrupted to mean "additional but not necessarily different" as opposed "different."

Claim 9 is indefinite as to what is or is not a "collagen-like" domain. In addition it is not clear what is or is not a "complement related protein" with regards to both structure and function.

Claim 10 is indefinite regarding overlapping members of the Markush group (See explanation is discussion above, claim 6). See same issue in claim 12.

Claim 11 is indefinite as the nucleotides are not distinct one from the other as ranges overlap.

Claim 12 is objected to because improper Markush language is recited in the claim. The claim should recite "an amino acid sequence selected from the group consisting of." The claim as stated recites a vector that consist of all DNA segments listed (a)-(h) in the claim.

Claims 13-15 are indefinite for being dependent from indefinite claims and do not correct issue of the indefinite claims.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

Claims 6, 8, 10, 11 and dependent claims thereto are rejected under 35 U.S.C. 102(a) as being anticipated by Bridgeman (Accession Number: Z82198). Bridgeman discloses a human nucleotide sequence that is identical to SEQ ID NO: 1 between the base pairs 98 and 1381.

Thus, the sequence anticipates the nucleic acid molecules consisting of base pairs 179-448 and 137-448 of SEQ ID NO: 1 recited in claim 11. Furthermore, the nucleic acid of Bridgeman would encode for the polypeptide comprising amino acid residues 60-149 and 46-149 of SEQ ID NO: 2 recited in claims 6, 8 and 10. As written, the use of "consisting" in claims 10 and 11 may be interpreted as "open" language. Thus, the reference anticipates the claimed invention.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claims 12-15 are rejected under 35 U.S.C. 103(a) as being unpatentable over Bridgeman (Accession Number: Z82198) in view of Lee *et al.* (Biotechnol Prog. 1999). Bridgeman discloses a human nucleotide sequence that is identical to SEQ ID NO: 1 between the base pairs 98 and 1381. This nucleic acid would encode for the polypeptide comprising amino acid residues 60-149 and 46-149 of SEQ ID NO: 2 recited in claim 12. Bridgeman does not teach an expression vector, host cell or method of isolating a polypeptide.

Lee *et al.* teach an expression system comprising of expression vector, secretory enhancer sequence and cultured cells. Lee *et al.* teach the insertion of a polynucleotide into the expression vector. The expression vector contains a secretory enhancer sequence operably linked to the DNA of interest that promotes the secretion of the synthesized protein of interest into the culture

media. Lee *et al.* additionally teach the introduction of the vector into cultured cells, culturing of the cells and how to produce and isolated the recombinant protein.

It would have been obvious to the person of ordinary skill in the art at the time the invention was made to insert the known nucleic acid molecule encoding for the polypeptide comprising amino acids 60-149 and 46-149 of SEQ ID NO: 2 into an expression vector taught by Lee *et al.* (claim 12). The expression vector of Lee *et al.* contains a secretory signal operably linked to the DNA segment of interest (claim 13). It would have been obvious to the person of ordinary skill in the art at the time the invention was made to introduce of the expression vector to a cultured cell and then to utilize that cell in a method of producing and isolating the polypeptide (claims 14 and 15).

The person of ordinary skill in the art would have been motivated, and reasonably would have expected success, to insert the known nucleic acid into an expression vector comprising a secretory signal because such expression vectors are used in the art to produce recombinant protein (Lee *et al.*). Thus, the claimed invention was within the ordinary skill in the art to make and use at the time it was made and was as a whole, *prima facie* obvious.

Advisory Information

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Sheridan K Snedden whose telephone number is (703) 305-4843. The examiner can normally be reached on Monday - Friday, 8:30 AM to 5:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christopher Low can be reached on (703) 308-2923. The fax phone numbers for the

organization where this application or proceeding is assigned are (703) 746-3975 for regular communications and (703) 746-3975 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

SKS
July 15, 2002
SKS

Christopher S. F. Low
CHRISTOPHER S. F. LOW
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 30, 2002, 12:22:13 ; Search time 1885.54 Seconds
(without alignments)
15326.934 Million cell updates/sec

Title: US-09-997-610-1
Perfect score: 1381
Sequence: 1 gatagtggtcatacctgtct.....tgtacctccattgtatgtag 1381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1284	93.0	145880	9	HS302D9	Z82198 Human DNA s
2	697.6	50.5	198545	2	AC017063	AC017063 Homo sapi
c 3	693.4	50.2	124518	9	AL138962	AL138962 Human DNA
4	693.2	50.2	77405	2	AL353634	AL353634 Homo sapi
5	692.6	50.2	40714	9	HSU212C1	Z69722 Human DNA s
6	690.8	50.0	123070	2	AC008799	AC008799 Homo sapi
c 7	690.8	50.0	189768	2	AC044889	AC044889 Homo sapi
8	689	49.9	154090	9	AC025577	AC025577 Homo sapi
9	689	49.9	186660	2	AC026107	AC026107 Homo sapi
c 10	686.6	49.7	170368	9	AC091982	AC091982 Homo sapi
11	686	49.7	67984	9	AC010312	AC010312 Homo sapi
c 12	684	49.5	168502	9	AC091005	AC091005 Homo sapi
c 13	682.4	49.4	73390	9	AC012038	AC012038 Homo sapi
14	681.6	49.4	131215	9	AC079614	AC079614 Homo sapi
15	681.4	49.3	173480	9	CNS00M8T	AL079343 Human chr
16	681	49.3	38235	9	AC004559	AC004559 Homo sapi
c 17	681	49.3	146743	2	AC093588	AC093588 Homo sapi
c 18	681	49.3	166679	9	AC079899	AC079899 Homo sapi
c 19	681	49.3	176426	9	AC007370	AC007370 Homo sapi
c 20	680.6	49.3	152544	9	CNS05TEJ	AL359232 Human chr
c 21	680.6	49.3	203726	2	AC011882	AC011882 Homo sapi
c 22	679.6	49.2	124531	9	HS0633H17	AL049710 Human DNA
c 23	679.2	49.2	187898	2	AC016715	AC016715 Homo sapi
c 24	679	49.2	138271	9	AC006360	AC006360 Homo sapi
25	679	49.2	147971	9	HS431P23	AL009178 Human DNA
26	678.2	49.1	107885	9	AC006389	AC006389 Homo sapi
c 27	678.2	49.1	150332	9	AC004921	AC004921 Homo sapi
c 28	678	49.1	181842	2	AL391823	AL391823 Homo sapi
29	677.8	49.1	77774	9	AP000339	AP000339 Homo sapi
30	677.8	49.1	84730	9	AP000230	AP000230 Homo sapi
31	677.8	49.1	100000	9	AP000144	AP000144 Homo sapi
32	677.8	49.1	100000	9	AP000217	AP000217 Homo sapi
33	677.8	49.1	100634	9	AP001594	AP001594 Homo sapi
34	677.8	49.1	340000	9	AP001695	AP001695 Homo sapi
35	677.8	49.1	340000	9	AP001760	AP001760 Homo sapi
c 36	677.6	49.1	155764	9	AC011238	AC011238 Homo sapi
c 37	677.4	49.1	182972	2	AC023550	AC023550 Homo sapi
c 38	676.4	49.0	125295	2	AL672061	AL672061 Homo sapi
c 39	676.4	49.0	174662	2	AC026036	AC026036 Homo sapi
40	676.2	49.0	123631	9	HS22F01	AL109967 Homo sapi
c 41	676.2	49.0	168863	9	AC011286	AC011286 Homo sapi
42	676	49.0	105692	9	AL451046	AL451046 Human DNA
43	676	49.0	135623	2	AC022618	AC022618 Homo sapi
c 44	675.8	48.9	239008	2	AC022460	AC022460 Homo sapi
45	675.4	48.9	150001	9	AC006063	AC006063 Homo sapi

ALIGNMENTS

RESULT 1
HS302D9
LOCUS HS302D9 145880 bp DNA linear PRI 12-DEC-1999
DEFINITION Human DNA sequence from clone RP1-302D9 on chromosome 22 Contains GSSs, complete sequence.
ACCESSION Z82198
VERSION Z82198.2 GI:6572207
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 145880)
AUTHORS Bridgeman,A.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Dec 13, 1999 this sequence version replaced gi:3164067.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22
RP1-302D9 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
This sequence is the entire insert of clone RP1-302D9 The true left end of clone CTA-282F2 is at 69682 in this sequence. The true right end of clone CTA-415G2 is at 55167 in this sequence.

FEATURES Location/Qualifiers

source	1. .145880
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="22"
	/clone="RP1-302D9"
	/clone_lib="RPCI-1"
repeat_region	188. .245
	/note="MER3 repeat: matches 144. .209 of consensus"
repeat_region	246. .571
	/note="AluSx repeat: matches 1. .312 of consensus"
repeat_region	572. .759
	/note="MER3 repeat: matches 1. .144 of consensus"
repeat_region	783. .933
	/note="MER5A repeat: matches 26. .187 of consensus"
repeat_region	1033. .1336
	/note="AluSp repeat: matches 1. .299 of consensus"
repeat_region	1450. .1583
	/note="MIR repeat: matches 24. .160 of consensus"
repeat_region	1687. .1752
	/note="L2 repeat: matches 2593. .2661 of consensus"
repeat_region	2350. .2660
	/note="AluSc repeat: matches 3. .309 of consensus"
repeat_region	2684. .2981
	/note="AluSq repeat: matches 2. .300 of consensus"
repeat_region	3323. .3343
	/note="MLT1E repeat: matches 116. .136 of consensus"
repeat_region	3344. .3652
	/note="AluY repeat: matches 1. .309 of consensus"
repeat_region	3653. .3928
	/note="MLT1E repeat: matches 136. .359 of consensus"
repeat_region	3929. .4278
	/note="THE1B repeat: matches 3. .364 of consensus"
repeat_region	4279. .4485
	/note="MLT1E repeat: matches 359. .568 of consensus"
repeat_region	5073. .5176
	/note="52 copies 2 mer ct 78 conserved"
repeat_region	5181. .5491
	/note="AluJb repeat: matches 1. .311 of consensus"
repeat_region	6369. .6485
	/note="L2 repeat: matches 2579. .2705 of consensus"
repeat_region	6647. .6685
	/note="MADE1 repeat: matches 1. .23 of consensus"
repeat_region	6686. .6987
	/note="AluSx repeat: matches 1. .302 of consensus"
repeat_region	6988. .7036
	/note="MADE1 repeat: matches 23. .77 of consensus"
repeat_region	7482. .7754
	/note="AluJb repeat: matches 9. .290 of consensus"
repeat_region	7775. .8060
	/note="AluJo repeat: matches 1. .295 of consensus"
repeat_region	8414. .8551
	/note="L2 repeat: matches 2553. .2706 of consensus"
repeat_region	8914. .9030
	/note="MIR repeat: matches 147. .262 of consensus"
repeat_region	9110. .9280
	/note="MIR repeat: matches 91. .262 of consensus"
repeat_region	9283. .9412
	/note="MIR repeat: matches 15. .144 of consensus"
repeat_region	9521. .9679
	/note="FAM repeat: matches 3. .161 of consensus"
repeat_region	9820. .10225
	/note="MSTB repeat: matches 2. .425 of consensus"
misc_feature	complement(10179. .10678)
	/note="match: GSS: Em:B56592"
misc_feature	complement(10204. .10728)
	/note="match: GSS: Em:AQ701486"
misc_feature	complement(10249. .10706)
	/note="match: GSS: Em:AQ225495"
repeat_region	10312. .10383
	/note="MIR repeat: matches 79. .150 of consensus"
misc_feature	10718. .11310
	/note="match: GSS: Em:B14024"
misc_feature	10784. .11201
	/note="match: GSS: Em:B43656"
repeat_region	11838. .11946
	/note="MIR repeat: matches 20. .137 of consensus"
repeat_region	12174. .12445
	/note="L2 repeat: matches 1988. .2275 of consensus"
repeat_region	12444. .12642
	/note="MIR repeat: matches 63. .241 of consensus"
misc_feature	13017. .13369
	/note="match: STS: Em:G49301"
repeat_region	13331. .13397
	/note="MIR repeat: matches 174. .244 of consensus"
repeat_region	13398. .13698
	/note="AluSp repeat: matches 1. .302 of consensus"
repeat_region	13699. .13810
	/note="MIR repeat: matches 76. .174 of consensus"
repeat_region	13806. .13919
	/note="MIR repeat: matches 77. .189 of consensus"
repeat_region	13945. .14060
	/note="MIR repeat: matches 24. .142 of consensus"
repeat_region	14061. .14367
	/note="AluY repeat: matches 1. .301 of consensus"
repeat_region	14368. .14452
	/note="MIR repeat: matches 141. .225 of consensus"
repeat_region	14589. .14679
	/note="MIR repeat: matches 173. .262 of consensus"
misc_feature	14597. .15201
	/note="match: GSS: Em:AQ553482"
misc_feature	14616. .15060
	/note="match: GSS: Em:AQ370601"
repeat_region	14868. .15040
	/note="MIR repeat: matches 49. .233 of consensus"
repeat_region	15071. .15188
	/note="L2 repeat: matches 2112. .2239 of consensus"
repeat_region	15304. .15399
	/note="MLT1B repeat: matches 1. .99 of consensus"
repeat_region	15490. .15662
	/note="AluSg1 repeat: matches 2. .114 of consensus"
repeat_region	15669. .15727
	/note="MLT1B repeat: matches 119. .178 of consensus"
repeat_region	15728. .16027
	/note="AluSc repeat: matches 1. .299 of consensus"
repeat_region	16028. .16245
	/note="MLT1B repeat: matches 178. .390 of consensus"
repeat_region	16546. .16854
	/note="AluY repeat: matches 1. .300 of consensus"
repeat_region	18296. .18323
	/note="MSTA repeat: matches 2. .29 of consensus"
repeat_region	18324. .18392

```
                     /note="MER66-internal repeat: matches 4919. .4993 of
                     consensus"
     repeat_region   18393. .18712
                     /note="AluJb repeat: matches 1. .311 of consensus"
     repeat_region   18713. .19133
                     /note="MER66-internal repeat: matches 4548. .4919 of
                     consensus"
     misc_feature    complement(18872. .19230)
                     /note="match: GSS: Em:AQ005063"
     misc_feature    19251. .19719
                     /note="match: GSS: Em:B14179"
     repeat_region   19537. .20290
                     /note="HERVFH21 repeat: matches 4657. .5784 of consensus"
     repeat_region   20317. .20382
                     /note="33 copies 2 mer ta 68 conserved"
     repeat_region   20513. .20666
                     /note="77 copies 2 mer tt 70 conserved"
     repeat_region   20682. .21008
                     /note="AluSg1 repeat: matches 1. .306 of consensus"
     repeat_region   21239. .21553
                     /note="HUERS-P3 repeat: matches 4410. .4713 of consensus"
     repeat_region   21882. .22254
                     /note="THE1B repeat: matches 1. .364 of consensus"
     repeat_region   22302. .22537
                     /note="MER66-internal repeat: matches 2186. .2417 of
                     consensus"
     repeat_region   22538. .22850
                     /note="AluSp repeat: matches 1. .313 of consensus"
     repeat_region   22851. .23801
                     /note="MER66-internal repeat: matches 1210. .2186 of
                     consensus"
     repeat_region   23905. .23989
                     /note="MER66-internal repeat: matches 3017. .3102 of

  Query Match             93.0%;  Score 1284;  DB 9;  Length 145880;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1287;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      90 tggggcctcctggtgcaccaggtttaccacaatatacaggagaaataagtgaaatgacaa 149
           |||    ||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   37254 TGGAATGTCCTGGTGCCCCAGGTTTACCACAATATACAGGAGAAATAAGTGAAATGACAA 37313

Qy     150 aatgcccctgtcctgatatagaaaggtcagcctttactgtgaagctcagtggaaaacttc 209
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   37314 AATGCCCCTGTCCTGATATAGAAAGGTCAGCCTTTACTGTGAAGCTCAGTGGAAAACTTC 37373

Qy     210 ctcttcctttcaagcccatcatcttcacaggggtcctgtacaatgcccagagggatttaa 269
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   37374 CTCTTCCTTTCAAGCCCATCATCTTCACAGGGGTCCTGTACAATGCCCAGAGGGATTTAA 37433

Qy     270 aggaggccatgggagtctttgcttgcagggtgcctgggaattactactccagctttgatg 329
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   37434 AGGAGGCCATGGGAGTCTTTGCTTGCAGGGTGCCTGGGAATTACTACTCCAGCTTTGATG 37493

Qy     330 ttgagctgcatcattgcaaggtgaatatttggctaatgaggaagcaaattttggctaata 389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   37494 TTGAGCTGCATCATTGCAAGGTGAATATTTGGCTAATGAGGAAGCAAATTTTGGCTAATA 37553

Qy     390 aggaagaaatttctaagcagcaaagcattcaagaggtgacttgggtgctgttaaaggcat 449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   37554 AGGAAGAAATTTCTAAGCAGCAAAGCATTCAAGAGGTGACTTGGGTGCTGTTAAAGGCAT 37613

Qy     450 tcagtttcataagggaggcagagcataagagttcagaaaatttgcaccctgacaatgtga 509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   37614 TCAGTTTCATAAGGGAGGCAGAGCATAAGAGTTCAGAAAATTTGCACCCTGACAATGTGA 37673

Qy     510 taaaaaagaaaaacccatttttctgaggggaaattcaagctggctgcagaaatttgcatat 569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   37674 TAAAAAAGAAAAACCCATTTTCTGAGGGGAAATTCAAGCTGGCTGCAGAAATTTGCATAT 37733

Qy     570 gtaatgaggagctgaatgttaatcctcaagacaatggggaaaatatctcctggacatgtc 629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   37734 GTAATGAGGAGCTGAATGTTAATCCTCAAGACAATGGGGAAAATATCTCCTGGACATGTC 37793

Qy     630 agaggtcttcacagcagtccatcaaatcactggcctggaggcctaggagaaaatggtttt 689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   37794 AGAGGTCTTCACAGCAGTCCATCAAATCACTGGCCTGGAGGCCTAGGAGAAAATGGTTTT 37853

Qy     690 gtgggacaggcccagggtccctgtgctgtgtgcagcctagagacttggtgccctgtgtcc 749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   37854 GTGGGACAGGCCCAGGGTCCCTGTGCTGTGTGCAGCCTAGAGACTTGGTGCCCTGTGTCC 37913

Qy     750 cagttaattcagctgtggcttcagagggtgcaagccccaagccttggcagcttccaagtg 809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   37914 CAGTTAATTCAGCTGTGGCTTCAGAGGGTGCAAGCCCCAAGCCTTGGCAGCTTCCAAGTG 37973

Qy     810 gtgttgagcctgtgggtgcaaagaagtcaagaattgaggtttgggaacctccaatcagat 869
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   37974 GTGTTGAGCCTGTGGGTGCAAAGAAGTCAAGAATTGAGGTTTGGGAACCTCCAATCAGAT 38033

Qy     870 ttcagaagatatatggaaaccccctggatgcccaggcagaagtttgctgtaggggtggggt 929
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   38034 TTCAGAAGATATATGGAAACCCCTGGATGCCCAGGCAGAAGTTTGCTGTAGGGGTGGGGT 38093

Qy     930 cctcatggagaacctctgcaagggtagtacaaaagggaaatgttgggtgggagcccccac 989
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   38094 CCTCATGGAGAACCTCTGCAAGGGTAGTACAAAAGGGAAATGTTGGGTGGGAGCCCCCAC 38153

Qy     990 acagagtccccagtggggctccatctagtagagctgtgagaagaagtccaccatcctcca 1049
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   38154 ACAGAGTCCCCAGTGGGGCTCCATCTAGTAGAGCTGTGAGAAGAAGTCCACCATCCTCCA 38213

Qy    1050 gactccagaagggtagatccactgacagcttgcagcatgtgcctgaaaaatccacagaca 1109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   38214 GACTCCAGAAGGGTAGATCCACTGACAGCTTGCAGCATGTGCCTGAAAAATCCACAGACA 38273

Qy    1110 ctcagtgccagcctgtgaaagcagcagggatggagtctgtaccctacaaaaccgtagtgg 1169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   38274 CTCAGTGCCAGCCTGTGAAAGCAGCAGGGATGGAGTCTGTACCCTACAAAACCGTAGTGG 38333

Qy    1170 cagagctgaccaagaccgtgggaatctacctcttgcattgtcatgacctggacgtgagac 1229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   38334 CAGAGCTGACCAAGACCGTGGGAATCTACCTCTTGCATTGTCATGACCTGGACGTGAGAC 38393

Qy    1230 atggagtcaaaagagatcattttggagctttaagatttgactgccccactggatttcgga 1289
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   38394 ATGGAGTCAAAAGAGATCATTTTGGAGCTTTAAGATTTGACTGCCCCACTGGATTTCGGA 38453

Qy    1290 cttatatggggcccgtacccctttgttttggccaatttttccatttggaactgccgtat 1349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   38454 CTTATATGGGGCCCGTACCCCTTTGTTTTGGCCAATTTTTTCCATTTGGAACTGCCGTAT 38513

Qy    1350 ttacccaatgcctgtacctccattgtatgtag 1381
           |||||||||||||||||||||||||||||||
Db   38514 TTACCCAATGCCTGTACCTCCATTGTATGTAG 38545
```

```
RESULT   2
AC017063
LOCUS       AC017063               198545 bp    DNA     linear   HTG 02-NOV-2001
DEFINITION  Homo sapiens chromosome 4 clone RP11-354H17, WORKING DRAFT
            SEQUENCE, 4 unordered pieces.
ACCESSION   AC017063
VERSION     AC017063.7  GI:16596637
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 198545)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 198545)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
```